

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: UNITED STATES OF AMERICA; DEPT.  
OF HEALTH AND HUMAN SERVICES
- (ii) TITLE OF INVENTION: MOTILITY STIMULATING  
PROTEIN USEFUL IN CANCER DIAGNOSIS AND  
THERAPY
- (iii) NUMBER OF SEQUENCES: 69
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: MORGAN & FINNEGAN  
(B) STREET: 345 PARK AVENUE  
(C) CITY: NEW YORK  
(D) STATE: NEW YORK  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10154
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy Disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WordPerfect 5.1
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA  
(A) APPLICATION NUMBER: 08/346,455  
(B) FILING DATE: 28-NOV-1994
- (vii) PRIOR APPLICATION DATA  
(A) APPLICATION NUMBER: 08/249,182  
(B) FILING DATE: 25-MAY-1994
- (vii) PRIOR APPLICATION DATA  
(A) APPLICATION NUMBER: 07/822,043  
(B) FILING DATE: 17-JAN-1992
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: DOROTHY R. AUTH  
(B) REGISTRATION NUMBER: 36,434  
(C) DOCKET NUMBER: 2026-4149US3
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (212) 758-4800  
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T,490

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp His Val Ala Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Leu Asp Val Tyr Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Pro Ala Phe Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Ala Glu Val Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Pro Glu Glu Val Thr Arg Pro Asn Tyr Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr Asp Val Pro Trp Asn Glu Thr Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Val Pro Pro Phe Glu Asn Ile Glu Leu Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Asn Ser Met Gln Thr Val Phe Val Gly Tyr Gly  
1 5 10

Pro Thr Phe Lys  
15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Ile Glu His Leu Thr Ser Leu Asp Phe Phe Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val Asp  
1 5 10

Asp Ile Thr Leu Val Pro Glu Thr Leu Gly Arg  
15 20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTGGCAGCN ACRTGCCA

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGGCAYGTNG CTGCCAAC

18

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTGAAGGCA GGGTA

15

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAYCCTGCNT TYAAG

15

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTNACYTCY TCAGG

15

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCTGARGARG TNACC

15

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

NGTNGCRTCR AATGGCACRT C

21

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAYGTGCCAT TYGAYGCNAC N

21

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTDDATRTTS TCRAATGGGG G

21

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCCCCATTTG AGAACATCAA C

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTTNGTNGCN GTDATCCANA RGGGYTGGCC GCC

33

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCGGCCARC CCYTNTGGAT HACNGCNACN AAG

33

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTTRAAGGTG GGGCCRTAGC CCACRAAGAC TGTYTGCAT

39

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGCARACAG TCTTYGTGGG CTAYGGCCCC ACCTTYAAR

39

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gln Tyr Leu His Gln Tyr Gly Ser Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Val Leu Asn Tyr Phe  
1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Tyr Leu Asn Ala Thr  
1 5



(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

His Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Tyr Pro Glu Ile Leu Thr Pro Ala Asp Asn  
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Xaa Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser  
1 5 10  
Ser Pro

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Phe	Ala	Thr	Gly	Leu
1				5					10		
Tyr											

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val	Asn	Val	Ile	Ser	Gly	Pro	Ile	Asp	Asp	Tyr	Asp
1				5					10		
Tyr	Asp	Gly	Leu	His	Asp	Thr	Glu	Asp	Lys		
		15					20				

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (B) STRAIN:
- (C) INDIVIDUAL ISOLATE:
- (D) DEVELOPMENTAL STAGE:
- (E) HAPLOTYPE:
- (F) TISSUE TYPE:
- (G) CELL TYPE: Melanoma
- (H) CELL LINE: A2058
- (I) ORGANELLE:

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Putative protein  
sequence of A2058 Autotaxin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Cys	His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys	Thr	Ala	
1				5					10			
Arg	Gly	Trp	Glu	Cys	Thr	Lys	Asp	Arg	Cys	Gly	Glu	
		15					20					
Val	Arg	Asn	Glu	Glu	Asn	Ala	Cys	His	Cys	Ser	Glu	
25					30					35		
Asp	Cys	Leu	Ala	Arg	Gly	Asp	Cys	Cys	Thr	Asn	Tyr	
			40					45				
Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp	Val	Asp	
	50					55					60	
Asp	Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala	Glu	Cys	Pro	
				65						70		
Ala	Gly	Phe	Val	Arg	Pro	Pro	Leu	Ile	Ile	Phe	Ser	
		75					80					
Val	Asp	Gly	Phe	Arg	Ala	Ser	Tyr	Met	Lys	Lys	Gly	
85					90					95		
Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu	Arg	Ser	
			100					105				
Cys	Gly	Thr	His	Ser	Pro	Tyr	Met	Arg	Pro	Val	Tyr	
	110					115					120	
Pro	Thr	Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	
			125							130		
Thr	Gly	Leu	Tyr	Pro	Glu	Ser	His	Gly	Ile	Val	Gly	
		135					140					
Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala	Thr	Phe	
145					150					155		
His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	
			160					165				
Trp	Gly	Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	
	170					175					180	
Gln	Gly	Val	Lys	Ala	Gly	Thr	Phe	Phe	Trp	Ser	Val	
			185						190			
Val	Ile	Pro	His	Glu	Arg	Arg	Ile	Leu	Thr	Ile	Leu	
		195					200					
Arg	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg	Pro	Ser	
205					210					215		
Val	Tyr	Ala	Phe	Tyr	Ser	Glu	Gln	Pro	Asp	Phe	Ser	
			220					225				
Gly	His	Lys	Tyr	Gly	Pro	Phe	Gly	Pro	Glu	Glu	Ser	
	230					235					240	
Ser	Tyr	Gly	Ser	Pro	Phe	Thr	Pro	Ala	Lys	Arg	Pro	
			245						250			
Lys	Arg	Lys	Val	Ala	Pro	Lys	Arg	Arg	Gln	Glu	Arg	
		255					260					
Pro	Val	Ala	Pro	Pro	Lys	Lys	Arg	Arg	Arg	Lys	Ile	
265					270					275		
His	Arg	Met	Asp	His	Tyr	Ala	Ala	Glu	Thr	Arg	Gln	
			280					285				

Asp	Lys	Met	Thr	Asn	Pro	Leu	Arg	Glu	Ile	Asp	Lys
290						295					300
Ile	Val	Gly	Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu
				305						310	
Lys	Leu	Arg	Arg	Cys	Val	Asn	Val	Ile	Phe	Val	Gly
		315					320				
Asp	His	Gly	Met	Glu	Asp	Val	Thr	Cys	Asp	Arg	Thr
325					330					335	
Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	Asp	Asp
			340					345			
Ile	Thr	Leu	Val	Pro	Gly	Thr	Leu	Gly	Arg	Ile	Arg
350						355					360
Ser	Lys	Phe	Ser	Asn	Asn	Ala	Lys	Tyr	Asp	Pro	Lys
				365					370		
Ala	Ile	Ile	Ala	Asn	Leu	Thr	Cys	Lys	Lys	Pro	Asp
		375					380				
Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	Leu	Pro
385					390					395	
Lys	Arg	Leu	His	Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu
			400					405			
Asp	Ile	His	Leu	Leu	Val	Glu	Arg	Arg	Trp	His	Val
410						415					420
Ala	Arg	Lys	Pro	Leu	Asp	Val	Tyr	Lys	Lys	Pro	Ser
				425					430		
Gly	Lys	Cys	Phe	Phe	Gln	Gly	Asp	His	Gly	Phe	Asp
		435					440				
Asn	Lys	Val	Asn	Ser	Met	Gln	Thr	Val	Phe	Val	Gly
445					450					455	
Tyr	Gly	Pro	Thr	Phe	Lys	Tyr	Lys	Thr	Lys	Val	Pro
			460					465			
Pro	Phe	Glu	Asn	Ile	Glu	Leu	Tyr	Asn	Val	Met	Cys
470						475					480
Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	Asn	Gly
				485					490		
Thr	His	Gly	Ser	Leu	Asn	His	Leu	Leu	Arg	Thr	Asn
		495					500				
Thr	Phe	Arg	Pro	Thr	Met	Pro	Glu	Glu	Val	Thr	Arg
505					510					515	
Pro	Asn	Tyr	Pro	Gly	Ile	Met	Tyr	Leu	Gln	Ser	Asp
			520					525			
Asp	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	Val	Glu
530						535					540
Pro	Lys	Asn	Lys	Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu
				545					550		
His	Thr	Lys	Gly	Ser	Thr	Glu	Glu	Arg	His	Leu	Leu
		555					560				
Tyr	Gly	Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr	Arg	Tyr
565					570					575	
Asp	Ile	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	Gly	Tyr
			580					585			
Ser	Glu	Ile	Phe	Leu	Met	Leu	Leu	Trp	Thr	Ser	Tyr
590						595					600
Thr	Val	Ser	Lys	Gln	Ala	Glu	Val	Ser	Ser	Val	Pro
				605						610	

Asp	His	Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp	Val	Arg
		615					620				
Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr
625					630					635	
Lys	Asn	Asp	Lys	Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe
			640					645			
Pro	Pro	Tyr	Leu	Ser	Ser	Ser	Pro	Glu	Ala	Lys	Tyr
	650				655						660
Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro	Met	Tyr
			665						670		
Pro	Ala	Phe	Lys	Arg	Val	Trp	Asn	Tyr	Phe	Gln	Arg
		675					680				
Val	Leu	Val	Lys	Lys	Tyr	Ala	Ser	Glu	Arg	Asn	Gly
685					690					695	
Val	Asn	Val	Ile	Ser	Gly	Pro	Ile	Phe	Asp	Tyr	Asp
			700					705			
Tyr	Asp	Gly	Leu	His	Asp	Thr	Glu	Asp	Lys	Ile	Lys
	710					715					720
Gln	Tyr	Val	Glu	Gly	Ser	Ser	Ile	Pro	Val	Pro	Thr
				725					730		
His	Tyr	Tyr	Ser	Ile	Ile	Thr	Ser	Cys	Leu	Asp	Phe
		735					740				
Thr	Gln	Pro	Ala	Asp	Lys	Cys	Asp	Gly	Pro	Leu	Ser
745					750					755	
Val	Ser	Ser	Phe	Ile	Leu	Pro	His	Arg	Pro	Asp	Asn
			760					765			
Glu	Glu	Ser	Cys	Asn	Ser	Ser	Glu	Asp	Glu	Ser	Lys
	770					775					780
Trp	Val	Glu	Glu	Leu	Met	Lys	Met	His	Thr	Ala	Arg
				785					790		
Val	Arg	Asp	Ile	Glu	His	Leu	Thr	Ser	Leu	Asp	Phe
		795					800				
Phe	Arg	Lys	Thr	Ser	Arg	Ser	Tyr	Pro	Glu	Ile	Leu
805					810					815	
Thr	Leu	Lys	Thr	Tyr	Leu	His	Thr	Tyr	Glu	Ser	Glu
			820					825			

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(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2946
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
  - (B) STRAIN:

(C) INDIVIDUAL ISOLATE:  
(D) DEVELOPMENTAL STAGE:  
(E) HAPLOTYPE:  
(F) TISSUE TYPE:  
(G) CELL TYPE: Melanoma  
(H) CELL LINE: A2058  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Partial DNA Sequence  
of A2058 Autotaxin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCTGCCATGA	CTTTGATGAG	CTGTGTTTGA	AGACAGCCCCG	40
TGGCTGGGAG	TGTACTAAGG	ACAGATGTGG	AGAAGTCAGA	80
AATGAAGAAA	ATGCCTGTCA	CTGCTCAGAG	GACTGCTTGG	120
CCAGGGGAGA	CTGCTGTACC	AATTACCAAG	TGGTTTGCAA	160
AGGAGAGTCG	CATTGGGTTG	ATGATGACTG	TGAGGAAATA	200
AAGGCCGCAG	AATGCCCTGC	AGGGTTTGT	CGCCCTCCAT	240
TAATCATCTT	CTCCGTGGAT	GGCTTCCGTG	CATCATACAT	280
GAAGAAAGGC	AGCAAAGTCA	TGCCTAATAT	TGAAAACTA	320
AGGTCTTGTG	GCACACACTC	TCCCTACATG	AGGCCGGTGT	360
ACCCAATAA	AACCTTTCCT	AACTTATACA	CTTTGGCCAC	400
TGGGCTATAT	CCAGAATCAC	ATGGAATTGT	TGGCAATTCA	440
ATGTATGATC	CTGTATTTGA	TGCCACTTTT	CATCTGCGAG	480
GGCGAGAGAA	ATTTAATCAT	AGATGGTGGG	GAGGTCAACC	520
GCTATGGATT	ACAGCCACCA	AGCAAGGGGT	GAAAGCTGGA	560
ACATTCTTTT	GGTCTGTTGT	CATCCCTCAC	GAGCGGAGAA	600
TATTAACCAT	ATTGCGGTGG	CTCACCTGTC	CAGATCATGA	640
GAGGCCTTCG	GTCTATGCCT	TCTATTCTGA	GCAACCTGAT	680
TTCTCTGGAC	ACAAATATGG	CCCTTTCGGC	CCTGAGGAGA	720
GTAGTTATGG	CTCACCTTTT	ACTCCGGCTA	AGAGACCTAA	760
GAGGAAAGTT	GCCCCTAAGA	GGAGACAGGA	AAGACCAGTT	800
GCTCCTCCAA	AGAAAAGAAG	AAGAAAAATA	CATAGGATGG	840
ATCATTATGC	TGCGGAAACT	CGTCAGGACA	AAATGACAAA	880
TCCTCTGAGG	GAAATCGACA	AAATTGTGGG	GCAATTAATG	920
GATGGACTGA	AACAATAAAA	ACTGCGTCGG	TGTGTCAACG	960
TCATCTTTGT	CGGAGACCAT	GGAATGGAAG	ATGTCACATG	1000
TGATAGAACT	GAGTTCTTGA	GTAATTACCT	AACTAATGTG	1040
GATGATATTA	CTTTAGTGCC	TGGAACCTCTA	GGAAGAATTC	1080
GATCCAAATT	TAGCAACAAT	GCTAAATATG	ACCCCAAAGC	1120
CATTATTGCC	AATCTCACGT	GTAAAAAACC	AGATCAGCAC	1160
TTTAAGCCTT	ACTTGAAACA	GCACCTTCCC	AAACGTTTGC	1200
ACTATGCCAA	CAACAGAAGA	ATTGAGGATA	TCCATTTATT	1240
GGTGGAACGC	AGATGGCATG	TTGCAAGGAA	ACCTTTGGAT	1280
GTTTATAAGA	AACCATCAGG	AAAATGCTTT	TTCCAGGGAG	1320
ACCACGGATT	TGATAACAAG	GTCAACAGCA	TGCAGACTGT	1360
TTTTGTAGGT	TATGGCCCAA	CATTTAAGTA	CAAGACTAAA	1400
GTGCCTCCAT	TTGAAAACAT	TGAACTTTAC	AATGTTATGT	1440
GTGATCTCCT	GGGATTGAAG	CCAGCTCCTA	ATAATGGGAC	1480

CCATGGAAGT	TTGAATCATC	TCCTGCGCAC	TAATACCTTC	1520
AGGCCAACCA	TGCCAGAGGA	AGTTACCAGA	CCCAATTATC	1560
CAGGGATTAT	GTACCTTCAG	TCTGATTTTG	ACCTGGGCTG	1600
CACTTGTGAT	GATAAGGTAG	AGCCAAAGAA	CAAGTTGGAT	1640
GAACTCAACA	AACGGCTTCA	TACAAAAGGG	TCTACAGAAG	1680
AGAGACACCT	CCTCTATGGG	CGACCTGCAG	TGCTTTATCG	1720
GACTAGATAT	GATATCTTAT	ATCACACTGA	CTTTGAAAGT	1760
GGTTATAGTG	AAATATTCCT	AATGCTACTC	TGGACATCAT	1800
ATACTGTTTC	CAAACAGGCT	GAGGTTTCCA	GCGTTCCTGA	1840
CCATCTGACC	AGTTGCGTCC	GGCCTGATGT	CCGTGTTTCT	1880
CCGAGTTTCA	GTCAGAACTG	TTTGGCCTAC	AAAAATGATA	1920
AGAGACACCT	CTACGGATTC	CTCTTTCCTC	CTTATCTGAG	1960
CTCTTCACCA	GAGGCTAAAT	ATGATGCATT	CCTTGTAACC	2000
AATATGGTTC	CAATGTATCC	TGCTTTCAAA	CGGGTCTGGA	2040
ATTATTTCCA	AAGGGTATTG	GTGAAGAAAT	ATGCTTCGGA	2080
AAGAAATGGA	GTTAACGTGA	TAAGTGGACC	AATCTTCGAC	2120
TATGACTATG	ATGGCTTACA	TGACACAGAA	GACAAAATAA	2160
AACAGTACGT	GGAAGGCAGT	TCCATTCTCT	TTCCAACTCA	2200
CTACTACAGC	ATCATCACCA	GCTGTCTGGA	TTTCACTCAG	2240
CCTGCCGACA	AGTGTGACGG	CCCTCTCTCT	GTGTCTCTCT	2280
TCATCCTGCC	TCACCGGCCT	GACAAAGAGG	AGAGCTGCAA	2320
TAGCTCAGAG	GACGAATCAA	AATGGGTTAG	AGAACTCATG	2360
AAGATGCACA	CAGCTAGGGT	GCGTGACATT	GAACATCTCA	2400
CCAGCCTGGA	CTTCTTCCGA	AAGACCAGCC	GCAGCTACCC	2440
AGAAATCCTG	ACACTCAAGA	CATACCTGCA	TACATATGAG	2480
AGCGAGATTT	AACTTTCTGA	GCATCTGCAG	TACAGTCTTA	2520
TCAACTGGTT	GTATATTTTT	ATATTGTTTT	TGTATTTATT	2560
AATTTGAAAC	CAGGACATTA	AAAATGTTAG	TATTTTAATC	2600
CTGTACCAAA	TCTGACATAT	TATGCCTGAA	TGACTCCACT	2640
GTTTTTCTCT	AATGCTTGAT	TTAGGTAGCC	TTGTGTTCTG	2680
AGTAGAGCTT	GTAATAAATA	CTGCAGCTTG	AGAAAAAGTG	2720
GAAGCTTCTA	AATGGTGCTG	CAGATTTGAT	ATTTGCATTG	2760
AGGAAATATT	AATTTTCCAA	TGCACAGTTG	CCACATTTAG	2800
TCCTGTACTG	TATGGAAACA	CTGATTTTGT	AAAGTTGCCT	2840
TTATTTGCTG	TTAACTGTTA	ACTATGACAG	ATATATTTAA	2880
GCCTTATAAA	CCAATCTTAA	ACATAATAAA	TCACACATTC	2920
AGTTTTTAAA	AAAAAAAAAA	AAAAAA		2946

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 788
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:

(D) DEVELOPMENTAL STAGE:  
 (E) HAPLOTYPE:  
 (F) TISSUE TYPE:  
 (G) CELL TYPE: teratocarcinoma  
 (H) CELL LINE: N-tera 2D1  
 (I) ORGANELLE:

(ix) FEATURE:  
 (A) NAME/KEY:  
 (B) LOCATION:  
 (C) IDENTIFICATION METHOD:  
 (D) OTHER INFORMATION: N-tera 2D1 putative  
 ATX protein sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Cys	Asp	Asn	Leu	Cys	Lys	Ser	Tyr	Thr	Ser	Cys	Cys
1				5				10			
His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys	Thr	Ala	Arg
		15					20				
Ala	Trp	Glu	Cys	Thr	Lys	Asp	Arg	Cys	Gly	Glu	Val
25					30				35		
Arg	Asn	Glu	Glu	Asn	Ala	Cys	His	Cys	Ser	Glu	Asp
			40					45			
Cys	Leu	Ala	Arg	Gly	Asp	Cys	Cys	Thr	Asn	Tyr	Gln
50					55					60	
Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp	Val	Asp	Asp
			65					70			
Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala	Glu	Cys	Leu	Gln
		75				80					
Val	Asp	Ser	Pro	Ser	Ile	Asn	His	Leu	Leu	Arg	Gly
85					90					95	
Trp	Leu	Pro	Met	Thr	Ser	Tyr	Met	Lys	Lys	Gly	Ser
			100					105			
Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu	Arg	Ser	Cys
	110				115					120	
Gly	Thr	His	Ser	Pro	Tyr	Met	Arg	Pro	Val	Tyr	Pro
			125					130			
Thr	Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	Thr
		135				140					
Gly	Leu	Tyr	Pro	Glu	Ser	His	Gly	Ile	Val	Gly	Asn
145				150					155		
Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala	Thr	Phe	His
			160				165				
Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp
170					175					180	
Ala	Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	Gln
			185					190			
Arg	Gly	Glu	Ser	Trp	Asn	Ile	Leu	Leu	Val	Cys	Cys
		195				200					
His	Pro	Ser	Arg	Ala	Glu	Ile	Leu	Thr	Ile	Leu	Gln
205				210						215	
Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg	Pro	Ser	Val
			220				225				



Tyr	Ala	Phe	Tyr	Ser	Glu	Gln	Pro	Asp	Phe	Ser	Gly
	230					235					240
His	Lys	His	Met	Pro	Phe	Gly	Pro	Glu	Met	Pro	Asn
				245					250		
Pro	Leu	Arg	Glu	Met	His	Lys	Ile	Val	Gly	Gln	Leu
		255					260				
Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	His	Arg	Cys
265					270					275	
Val	Asn	Val	Ile	Phe	Val	Glu	Thr	Met	Asp	Gly	Arg
			280					285			
Cys	His	Met	Tyr	Arg	Thr	Glu	Phe	Leu	Ser	Asn	Tyr
	290					295					300
Leu	Thr	Asn	Val	Asp	Asp	Ile	Thr	Leu	Val	Pro	Gly
				305					310		
Thr	Leu	Gly	Arg	Ile	Arg	Ser	Lys	Phe	Ser	Asn	Asn
		315					320				
Ala	Lys	Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu
325					330					335	
Thr	Cys	Lys	Lys	Pro	Asp	Gln	His	Phe	Lys	Pro	Tyr
			340					345			
Leu	Lys	Gln	His	Leu	Pro	Lys	Arg	Leu	His	Tyr	Ala
	350					355					360
Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	His	Leu	Leu	Val
				365					370		
Glu	Arg	Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp
		375					380				
Val	Tyr	Lys	Lys	Pro	Ser	Gly	Asn	Ala	Phe	Ser	Arg
385					390					395	
Glu	Thr	Thr	Ala	Phe	Asp	Asn	Lys	Val	Asn	Ser	Met
			400					405			
Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	Pro	Thr	Phe	Lys
	410					415					420
Tyr	Lys	Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu
				425					430		
Leu	Tyr	Asn	Val	Met	Cys	Asp	Leu	Leu	Gly	Leu	Lys
		435					440				
Pro	Ala	Pro	Asn	Asn	Gly	Thr	His	Phe	Ser	Leu	Asn
445					450					455	
His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	Arg	Pro	Thr	Met
			460					465			
Pro	Glu	Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile
	470					475					480
Met	Tyr	Leu	Gln	Ser	Asp	Phe	Asp	Leu	Gly	Cys	Thr
				485					490		
Cys	Asp	Asp	Lys	Val	Glu	Pro	Lys	Asn	Lys	Leu	Asp
		495					500				
Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	Lys	Gly	Ser	Thr
505					510					515	
Glu	Glu	Arg	His	Leu	Leu	Tyr	Gly	Asp	Arg	Pro	Ala
			520					525			
Val	Leu	Tyr	Arg	Thr	Arg	Tyr	Asp	Ile	Leu	Tyr	His
	530					535					540
Thr	Asp	Phe	Glu	Ser	Gly	Tyr	Ser	Glu	Ile	Phe	Leu
				545						550	

Met	Pro	Leu	Trp	Thr	Ser	Tyr	Thr	Val	Ser	Lys	Gln
		555					560				
Ala	Glu	Val	Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser
565					570					575	
Cys	Val	Arg	Pro	Asp	Val	Arg	Val	Ser	Pro	Ser	Phe
			580					585			
Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn	Asp	Lys	Gln
	590					595					600
Met	Ser	Tyr	Gly	Gly	Leu	Gly	Pro	Pro	Tyr	Leu	Ser
			605						610		
Ser	Ser	Pro	Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val
		615					620				
Thr	Asn	Met	Val	Pro	Met	Tyr	Pro	Ala	Phe	Lys	Arg
625					630					635	
Val	Trp	Asn	Tyr	Phe	Gln	Arg	Val	Leu	Val	Lys	Lys
			640					645			
Tyr	Ala	Ser	Glu	Arg	Asn	Gly	Val	Asn	Val	Ile	Ser
	650					655					660
Gly	Pro	Ile	Phe	Asp	Tyr	Asp	Tyr	Asp	Gly	Leu	His
			665						670		
Asp	Thr	Glu	Asp	Lys	Ile	Lys	Gln	Tyr	Val	Glu	Gly
		675					680				
Ser	Ser	Ile	Pro	Val	Pro	Thr	His	Tyr	Tyr	Ser	Ile
685					690					695	
Ile	Thr	Ser	Cys	Leu	Asp	Phe	Thr	Gln	Pro	Ala	Asp
			700					705			
Lys	Cys	Asp	Gly	Pro	Leu	Ser	Val	Ser	Ser	Phe	Ile
	710					715					720
Leu	Pro	His	Arg	Pro	Asp	Asn	Glu	Glu	Ser	Cys	Asn
				725					730		
Ser	Ser	Glu	Asp	Glu	Ser	Lys	Trp	Val	Glu	Glu	Leu
		735					740				
Met	Lys	Met	His	Thr	Ala	Arg	Val	Arg	Asp	Ile	Glu
745					750					755	
His	Leu	Thr	Ser	Leu	Asp	Phe	Phe	Arg	Lys	Thr	Ser
			760					765			
Arg	Ser	Tyr	Pro	Glu	Ile	Leu	Thr	Leu	Lys	Thr	Tyr
	770					775					780
Leu	His	Thr	Tyr	Glu	Ser	Glu	Ile				
				785							

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2712
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Human  
 (B) STRAIN:  
 (C) INDIVIDUAL ISOLATE:  
 (D) DEVELOPMENTAL STAGE:  
 (E) HAPLOTYPE:  
 (F) TISSUE TYPE:  
 (G) CELL TYPE: teratocarcinoma  
 (H) CELL LINE: N-tera 2D1  
 (I) ORGANELLE:

(ix) FEATURE:  
 (A) NAME/KEY:  
 (B) LOCATION:  
 (C) IDENTIFICATION METHOD:  
 (D) OTHER INFORMATION: N-tera 2D1 ATX DNA sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGTGACAACT	TGTGTAAGAG	CTATACCACT	TGCTGCCATG	40
ACTTTGATGA	GCTGTGTTT	AAGACAGCCC	GTGCGTGGGA	80
GTGTACTAAG	GACAGATGTG	GGGAAGTCAG	AAATGAAGAA	120
AATGCCTGTC	ACTGCTCAGA	GGACTGCTTG	GCCAGGGGAG	160
ACTGCTGTAA	CAATTACCAA	GTGGTTTGCA	AAGGAGAGTC	200
GCATTGGGTT	GATGATGACT	GTGAGGAAAT	AAAGGCCGCA	240
GAATGCCTGC	AGGTTTGTTT	GCCCTCCATT	AATCATCTTC	280
TCCGTGGATG	GCTTCCGATG	ACATCATACA	TGAAGAAAGG	320
CAGCAAAGTC	ATGCCTAATA	TTGAAAAACT	AAGGTCTTGT	360
GGCACACACT	CTCCCTACAT	GAGGCCGGTG	TACCCAACTA	400
AAACCTTTCC	TAACTTATAC	ACTTTGGCCA	CTGGGCTATA	440
TCCAGAATCA	CATGGAATTG	TTGGCAATTC	AATGTATGAT	480
CCTGTATTTG	ATGCCACTTT	TCATCTGCGA	GGGCGAGAGA	520
AATTTAATCA	TAGATGGTGG	GGAGGTCAAC	CGCTATGGAT	560
TACAGCCACC	AAGCAAAGGG	GTGAAAGCTG	GAACATTCTT	600
TTGGTCTGTT	GTCATCCCTC	ACGAGCGGAG	ATATTAACCA	640
TATTGCAGTG	GCTCACCCCTG	CCAGATCATG	AGAGGCCTTC	680
GGTCTATGCC	TTCTATTCTG	AGCAACCTGA	TTTCTCTGGA	720
CACAAACATA	TGCCTTTTCGG	CCCTGAGATG	ACAAATCCTC	760
TGAGGGGAAAT	GCACAAAATT	GTGGGGCAAT	TAATGGATGG	800
ACTGAAACAA	CTAAAACCTGC	ATCGGTGTGT	CAACGTCATC	840
TTTGTCGAGA	CCATGGATGG	AAGATGTCAC	ATGTATAGAA	880
CTGAGTTCTT	GAGTAATTAC	CTAACTAATG	TGGATGATAT	920
TACTTTAGTG	CCTGGAACCTC	TAGGAAGAAT	TCGATCCAAA	960
TTTAGCAACA	ATGCTAAATA	TCACCCCAAA	GCCATTATTG	1000
CCAATCTCAC	GTGTAAAAAA	CCAGATCAGC	ACTTTAAGCC	1040
TTACTTGAAA	CAGCACCTTC	CCAAACGTTT	GCACTATGCC	1080
AACAACAGAA	GAATTGAGGA	TATCCATTTA	TTGGTGGAAC	1120
GCAGATGGCA	TGTTGCAAGG	AAACCTTTTG	ATGTTTATAA	1160
GAAACCATCA	GGAAATGCTT	TTTCCAGGGA	GACCACGGCA	1200
TTTGATAACA	AGGTCAACAG	CATGCAGACT	GTTTTTGTAG	1240
GTTATGGCCC	AACATTTAAG	TACAAGACTA	AAGTDCCTCC	1280
ATTTGAAAAC	ATTGAACTTT	AAAATGTTAT	GTGTGATCTC	1320

CTGGGATTGA	AGCCAGCTCC	TAATAATGGG	ACCCATGGAA	1360
GTTTGAATCA	TCTCCTGCGC	ACTAATACCT	TCAGGCCAAC	1400
CATGCCAGAG	GAAGTTACCA	GACCCTATTA	TCCAGGGATT	1440
ATGTACCTTC	AGTCTGATTT	TGACCTGGGC	TGCACTTGTTG	1480
ATGATAAGGT	AGAGCCAAAG	AACAAGTTGG	ATGAACTCAA	1520
CAAACGGCTT	CATACAAAAG	GGTCTACAGA	AGAGAGACAC	1560
CTCCTCTATG	GGGATCGACC	TGCAGTGCTT	TATCGGACTA	1600
GATATGATAT	CTTATATCAC	ACTGACTTTG	AAAGTGGTTA	1640
TAGTGAAATA	TTCCTAATGC	CACTCTGGAC	ATCATATACT	1680
GTTTCCAAAC	AGGCTGAGGT	TTCCAGCGTT	CCTGACCATC	1720
TGACCAGTTG	CGTCCGGCCT	GATGTCCGTG	TTTCTCCGAG	1760
TTTCAGTTCAG	AACTGTTTGG	CCTACAAAAA	TGATAAGCAG	1800
ATGTCCTACG	GATTCCCTCTT	TCCTCCTTAT	CTGAGCTCTT	1840
CACCAGAGGC	TAAATATGAT	GCATTCCCTG	TAACCAATAT	1880
GGTTCCAATG	TATCCTGCTT	TCAAACGGGT	CTGGAATTAT	1920
TTCCAAAGGG	TATTGGTGAA	GAAATATGCT	TCGGAAAGAA	1960
ATGGAGTTAA	CGTGATAAGT	GGACCAATCT	TCGACTATGA	2000
CTATGATGGC	TTACATGACA	CAGAAGACAA	AATAAAACAG	2040
TACGTGGAAG	GCAGTTCCAT	TCCTGTTCCA	ACTCACTACT	2080
ACAGCATCAT	CACCAGCTGT	CTGGATTTCA	CTCAGCCTGC	2120
CGACAAGTGT	GACGGCCCTC	TCTCTGTGTC	CTCCTTCATC	2160
CTGCCTCACC	GGCCTGACAA	CGAGGAGAGC	TGCAATAGCT	2200
CAGAGGACGA	ATCAAAATGG	GTAGAAGAAC	TCATGAAGAT	2240
GCACACAGCT	AGGGTGCGTG	ACATTGAACA	TCTCACCAGC	2280
CTGGACTTCT	TCCGAAAGAC	CAGCCGCAGC	TACCCAGAAA	2320
TCCTGACACT	CAAGACATAC	CTGCATACAT	ATGAGAGCGA	2360
GATTTAACTT	TCTGAGCATC	TGCAGTACAG	TCTTATCAAC	2400
TGGTTGTATA	TTTTTATATT	GTTTTTGTAT	TTATTAATTT	2440
GAAACCAGGA	CATTAAAAAT	GTTAGTATTT	TAATCCTGTA	2480
CCAAATCTGA	CATATTATGC	CTGAATGACT	CCACTGTTTT	2520
TCTCTAATGC	TTGATTTAGG	TAGCCTTGTTG	TTCTGAGTAG	2560
AGCTTGTAAT	AAATACTGCA	GCTTGAGTTT	TTAGTGGAAG	2600
CTTCTAAATG	GTGCTGCAGA	TTTGATATTT	GCATTGAGGA	2640
AATATTAATT	TTCCAATGCA	CAGTTGCCAC	ATTTAGTCCT	2680
GTACTGTATG	GAAACACTGA	TTTTGTAAAG	TT	2712

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 979
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: No
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:

(F) TISSUE TYPE: Liver  
(G) CELL TYPE:  
(H) CELL LINE:  
(I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: putative autotaxin  
protein sequence from human liver

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Ala	Arg	Arg	Ser	Ser	Phe	Gln	Ser	Cys	Gln	Asp
1				5					10		
Ile	Ser	Leu	Phe	Thr	Phe	Ala	Val	Gly	Val	Asn	Ile
		15					20				
Cys	Leu	Gly	Phe	Thr	Ala	His	Arg	Ile	Lys	Arg	Ala
25					30					35	
Glu	Gly	Trp	Glu	Glu	Gly	Pro	Pro	Thr	Val	Leu	Ser
			40					45			
Asp	Ser	Pro	Trp	Thr	Asn	Ile	Ser	Gly	Ser	Cys	Lys
50					55					60	
Gly	Arg	Cys	Phe	Glu	Leu	Gln	Glu	Ala	Gly	Pro	Pro
			65						70		
Asp	Cys	Arg	Cys	Asp	Asn	Leu	Cys	Lys	Ser	Tyr	Thr
		75				80					
Ser	Cys	Cys	His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys
85				90						95	
Thr	Ala	Arg	Ala	Trp	Glu	Cys	Thr	Lys	Asp	Arg	Cys
			100					105			
Gly	Glu	Val	Arg	Asn	Glu	Glu	Asn	Ala	Cys	His	Cys
110					115					120	
Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly	Asp	Cys	Cys	Thr
			125						130		
Asn	Tyr	Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp
		135					140				
Val	Asp	Asp	Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala	Glu
145					150				155		
Cys	Leu	Gln	Val	Cys	Ser	Pro	Ser	Ile	Asn	His	Leu
			160					165			
Leu	Arg	Gly	Trp	Leu	Pro	Met	Thr	Ser	Tyr	Met	Lys
170					175					180	
Lys	Gly	Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu
			185						190		
Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	Tyr	Met	Arg	Pro
		195					200				
Val	Tyr	Pro	Thr	Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr
205					210				215		
Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu	Ser	His	Gly	Ile
			220					225			
Val	Gly	Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala
230						235					240

Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His	
				245					250			
Arg	Trp	Trp	Gly	Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	
		255					260					
Thr	Lys	Gln	Arg	Gly	Glu	Ser	Trp	Asn	Ile	Leu	Leu	
265					270					275		
Val	Cys	Cys	His	Pro	Ser	Arg	Ala	Glu	Ile	Leu	Thr	
			280					285				
Ile	Leu	Gln	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg	
	290					295					300	
Pro	Ser	Val	Tyr	Ala	Phe	Tyr	Ser	Glu	Gln	Pro	Asp	
				305					310			
Phe	Ser	Gly	His	Lys	His	Met	Pro	Phe	Gly	Pro	Glu	
		315					320					
Met	Thr	Asn	Pro	Leu	Arg	Glu	Met	His	Lys	Ile	Val	
325					330					335		
Gly	Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	
			340					345				
His	Arg	Cys	Val	Asn	Val	Ile	Phe	Val	Glu	Thr	Met	
	350					355					360	
Asp	Gly	Arg	Cys	His	Met	Tyr	Arg	Thr	Glu	Phe	Leu	
				365					370			
Ser	Asn	Tyr	Leu	Thr	Asn	Val	Asp	Asp	Ile	Thr	Leu	
		375					380					
Val	Pro	Gly	Thr	Leu	Gly	Arg	Ile	Arg	Ser	Lys	Phe	
385					390					395		
Ser	Asn	Asn	Ala	Lys	Tyr	Asp	Pro	Lys	Ala	Ile	Ile	
			400					405				
Ala	Asn	Leu	Thr	Cys	Lys	Lys	Pro	Asp	Gln	His	Phe	
	410					415					420	
Lys	Pro	Tyr	Leu	Lys	Gln	His	Leu	Pro	Lys	Arg	Leu	
				425					430			
His	Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	His	
		435					440					
Leu	Leu	Val	Glu	Arg	Arg	Trp	His	Val	Ala	Arg	Lys	
445					450					455		
Pro	Leu	Asp	Val	Tyr	Lys	Lys	Pro	Ser	Gly	Asn	Ala	
			460					465				
Phe	Ser	Arg	Glu	Thr	Thr	Ala	Phe	Asp	Asn	Lys	Val	
	470					475					480	
Asn	Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	Pro	
				485					490			
Thr	Phe	Lys	Tyr	Lys	Thr	Lys	Val	Pro	Pro	Phe	Glu	
		495					500					
Asn	Ile	Glu	Leu	Tyr	Asn	Val	Met	Cys	Asp	Leu	Leu	
505					510					515		
Gly	Leu	Lys	Pro	Ala	Pro	Asn	Asn	Gly	Thr	His	Gly	
			520					525				
Ser	Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	Arg	
	530					535					540	
Pro	Thr	Met	Pro	Glu	Glu	Val	Thr	Arg	Pro	Asn	Tyr	
				545					550			
Pro	Gly	Ile	Met	Tyr	Leu	Gln	Ser	Asp	Phe	Asp	Leu	
		555					560					

Gly	Cys	Thr	Cys	Asp	Asp	Lys	Val	Glu	Pro	Lys	Asn
565					570					575	
Lys	Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	Lys
			580					585			
Gly	Ser	Thr	Glu	Glu	Arg	His	Leu	Leu	Tyr	Gly	Asp
	590					595					600
Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr	Arg	Tyr	Asp	Ile
				605					610		
Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	Gly	Tyr	Ser	Glu
		615					620				
Ile	Phe	Leu	Met	Pro	Leu	Trp	Thr	Ser	Tyr	Thr	Val
625					630					635	
Ser	Lys	Gln	Ala	Glu	Val	Ser	Ser	Val	Pro	Asp	His
			640					645			
Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp	Val	Arg	Val	Ser
	650					655					660
Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn
				665					670		
Asp	Lys	Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe	Pro	Pro
		675					680				
Tyr	Leu	Ser	Ser	Ser	Pro	Glu	Ala	Lys	Tyr	Asp	Ala
685					690					695	
Phe	Leu	Val	Thr	Asn	Met	Val	Pro	Met	Tyr	Pro	Ala
			700					705			
Phe	Lys	Arg	Val	Trp	Asn	Tyr	Phe	Gln	Arg	Val	Leu
	710					715					720
Val	Lys	Lys	Tyr	Ala	Ser	Glu	Arg	Asn	Gly	Val	Asn
				725					730		
Val	Ile	Ser	Gly	Pro	Ile	Phe	Asp	Tyr	Asp	Tyr	Asp
		735					740				
Gly	Leu	His	Asp	Thr	Glu	Asp	Lys	Ile	Lys	Gln	Tyr
745					750					755	
Val	Glu	Gly	Ser	Ser	Ile	Pro	Val	Pro	Thr	His	Tyr
			760					765			
Tyr	Ser	Ile	Ile	Thr	Ser	Cys	Leu	Asp	Phe	Thr	Gln
	770					775					780
Pro	Ala	Asp	Lys	Cys	Asp	Gly	Pro	Leu	Ser	Val	Ser
				785					790		
Ser	Phe	Ile	Leu	Pro	His	Arg	Pro	Asp	Asn	Glu	Glu
		795					800				
Ser	Cys	Asn	Ser	Ser	Glu	Asp	Glu	Ser	Lys	Trp	Val
805					810					815	
Glu	Glu	Leu	Met	Lys	Met	His	Thr	Ala	Arg	Val	Arg
			820					825			
Asp	Ile	Glu	His	Leu	Thr	Ser	Leu	Asp	Phe	Phe	Arg
	830					835					840
Lys	Thr	Ser	Arg	Ser	Tyr	Pro	Glu	Ile	Leu	Thr	Leu
				845					850		
Lys	Thr	Tyr	Leu	His	Thr	Tyr	Glu	Ser	Glu	Ile	Xaa
		855					860				
Leu	Ser	Glu	His	Leu	Gln	Tyr	Ser	Leu	Ile	Asn	Trp
865					870					875	
Leu	Tyr	Ile	Phe	Ile	Leu	Phe	Leu	Tyr	Leu	Leu	Ile
			880					885			

Xaa	Asn	Gln	Asp	Ile	Lys	Asn	Val	Ser	Ile	Leu	Ile
	890					895					900
Leu	Tyr	Gln	Ile	Xaa	His	Ile	Met	Pro	Glu	Xaa	Leu
				905					910		
His	Cys	Phe	Ser	Leu	Met	Leu	Asp	Leu	Gly	Ser	Leu
		915					920				
Val	Phe	Xaa	Val	Glu	Leu	Val	Ile	Asn	Thr	Ala	Ala
925					930					935	
Xaa	Val	Phe	Ser	Gly	Ser	Phe	Xaa	Met	Val	Leu	Gln
			940					945			
Ile	Xaa	Tyr	Leu	His	Xaa	Gly	Asn	Ile	Asn	Phe	Pro
	950					955					960
Met	His	Ser	Cys	His	Ile	Xaa	Ser	Cys	Thr	Val	Trp
				965					970		
Lys	His	Xaa	Phe	Cys	Lys	Val					
				975							

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8
  - (B) TYPE: amino acids
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: peptide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY: ATX-204
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met His Thr Ala Arg Val Arg Asp  
5

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: No



- (ix) FEATURE:  
(A) NAME/KEY: ATX-205  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Phe Ser Asn Asn Ala Lys Tyr Asp  
5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7  
(B) TYPE: amino acids  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE:  
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

- (ix) FEATURE:  
(A) NAME/KEY: ATX-209  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Val Met Pro Asn Ile Glu Lys  
5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8  
(B) TYPE: amino acids  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE:  
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

- (ix) FEATURE:  
(A) NAME/KEY: ATX-210  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Ala Arg Gly Trp Glu Cys Thr  
5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:  
(A) NAME/KEY: ATX-212  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Xaa Asp Ser Pro Trp Thr Xaa Ile Ser Gly Ser  
5 10

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11  
(B) TYPE: amino acids  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:  
(A) NAME/KEY: ATX-214  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Leu Arg Ser Cys Gly Thr His Ser Pro Tyr Met  
5 10

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: Peptide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY: ATX-215/34A
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Thr Tyr Leu His Thr Tyr Glu Ser  
5

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13
  - (B) TYPE: amino acids
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: Peptide
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro Asp Gln  
5 10

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8  
(B) TYPE: amino acids  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: Peptide  
(iii) HYPOTHETICAL: No

(ix) FEATURE:  
(A) NAME/KEY: ATX-216  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ile Val Gly Gln Leu Met Asp Gly  
5

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9  
(B) TYPE: amino acids  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:  
(A) NAME/KEY: ATX-218/44  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Thr Ser Arg Ser Tyr Pro Glu Ile Leu  
5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9

(B) TYPE: amino acids  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No  
(ix) FEATURE:  
(A) NAME/KEY: ATX-223B/24  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Gln Ala Glu Val Ser Ser Val Pro Asp  
5

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14  
(B) TYPE: amino acids  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:  
(A) NAME/KEY: ATX-224  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Arg Cys Phe Glu Leu Gln Glu Ala Gly Pro Pro Asp Asp Cys  
5 10

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

(A) NAME/KEY: ATX-229

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu

5 10

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: Peptide

(iii) HYPOTHETICAL: No

(ix) FEATURE:

(A) NAME/KEY: ATX-224/53

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu

1 5 10

Ser Ser Ser Pro

15

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE:

(A) DESCRIPTION: cDNA

- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE:
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE: Liver
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: 5' end of human liver ATX gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGCAAGGA	GGAGCTCGTT	CCAGTCGTGT	CAAGATATAT	40
CCCTGTTCAC	TTTGCCGTT	GGAGTCAATA	TCTGCTTAGG	80
ATTCAGTGCA	CATCGAATTA	AGAGAGCAGA	AGGATGG	117

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39
  - (B) TYPE: amino acids
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: Peptide
- (iii) HYPOTHETICAL: No
- (v) FRAGMENT TYPE: N-terminal fragment
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Human
  - (B) STRAIN:
  - (C) INDIVIDUAL ISOLATE:
  - (D) DEVELOPMENTAL STAGE:
  - (E) HAPLOTYPE:
  - (F) TISSUE TYPE: Liver
  - (G) CELL TYPE:
  - (H) CELL LINE:
  - (I) ORGANELLE:

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: N-terminal region  
including transmembrane domain of liver  
ATX protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Asp
 1             5             10
Ile Ser Leu Phe Thr Phe Ala Val Gly Val Asn Ile
      15             20
Cys Leu Gly Phe Thr Ala His Arg Ile Lys Arg Ala
 25             30             35
Glu Gly Trp
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: Yes

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION: Primer from 5' end of  
4C11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCTCAGATAA GGAGGAAAGA G

21

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: Yes
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: Nested primers from 4C11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GAATCCGTAG GACATCTGCT T

21

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: Yes
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: Nested primers from 4C11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGTAGGCCAA ACAGTTCTGA C

21

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: Nested sense primer deduced from ATX-101, wherein N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAYTCNATGC ARACNGTNTT YGTNG

25

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: Nested primer of ATX -101, wherein N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTYGTNGGNT AYGGNCCNAC NTTYAA

26

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No

- (iv) ANTI-SENSE: No
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: Nested primer deduced from ATX-103, wherein N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AAYTAYCTNA CNAAYGTNGA YGAYAT

26

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: Nested primer deduced from ATX-103, wherein N is inosine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAYGAYATNA CNCTNGTNCC NGGNAC

26

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No

- (ix) FEATURE:  
    (A) NAME/KEY:  
    (B) LOCATION:  
    (C) IDENTIFICATION METHOD:  
    (D) OTHER INFORMATION: Nested primer deduced  
        from ATX-103, wherein N is inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TGYTTYGARY TNCARGARGC NGGNCCNCC

29

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCTGTCTTCA AACACAGC

18

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CTGGTGGCTG TAATCCATAG C

21

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION: Primer for 5' end of N-tera 2D1 sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CGTGAAGGCA AAGAGAACAC G

21

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3104
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY: N-tera 2D1 ATX cDNA
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AGTGCACTCC	GTGAAGGCAA	AGAGAACACG	CTGCAAAAGG	40
CTTTCCAATA	ATCCTCGACA	TGGCAAGGAG	GAGCTCGTTC	80
CAGTCGTGTC	AGATAATATC	CCTGTTCACT	TTTGCCGTTG	120
GAGTCAATAT	CTGCTTAGGA	TTCAGTGCAC	ATCGAATTAA	160
GAGAGCAGAA	GGATGGGAGG	AAGGTCCTCC	TACAGTGCTA	200
TCAGACTCCC	CCTGGACCAA	CATCTCCGGA	TCTTGCAAGG	240
GCAGGTGCTT	TGAACTTCAA	GAGGCTGGAC	CTCCTGATTG	280
TCGCTGTGAC	AACTTGTGTA	AGAGCTATAC	CAGTTGCTGC	320
CATGACTTTG	ATGAGCTGTG	TTTGAAGACA	GCCCGTGCGT	360
GGGAGTGTA	TAAGGACAGA	TGTGGAGAAG	TCAGAAATGA	400
AGAAAATGCC	TGTCAGTGCT	CAGAGGACTG	CTTGGCCAGG	440
GGAGACTGCT	GTACCAATTA	CCAAGTGGTT	TGCAAAGGAG	480
AGTCGCATTG	GGTTGATGAT	GACTGTGAGG	AAATAAAGGC	520
CGCAGAATGC	CCTGCAGGGT	TTGTTCGCC	TCCATTAATC	560

ATCTTCTCCG	TGGATGGCTT	CCGTGCATCA	TACATGAAGA	600
AAGGCAGCAA	AGTCATGCCT	AATATTGAAA	AACTAAGGTC	640
TTGTGGCACA	CACTCGCCCC	ACATGAGGCC	GGTGTACCCA	680
ACTAAAACCT	TTCCTAACTT	ATACACTTTG	GCCACTGGGC	720
TATATCCAGA	ATCACATGGA	ATTGTTGGCA	ATTCAATGTA	760
TGATCCTGTA	TTTGATGCCA	CTTTTCATCT	GCGAGGGCGA	800
GAGAAATTTA	ATCATAGATG	GTGGGGAGGT	CAACCGCTAT	840
GGATTACAGC	CACCAAGCAA	AGGGGTGAAA	GCTGGAACAT	880
TCTTTTGGTC	TGTTGTCATC	CCTCACGAGC	GGAGATATTA	920
ACCATATTGC	AGTGGCTCAC	CCTGCCAGAT	CATGAGAGGC	960
TTCGGTCTAT	GCCTTCTATT	CTGAGCAACC	TGATTTCTCT	1000
GGACACAAAT	ATGCCTTTTCG	GCCCTGAGAT	GACAAATCCT	1040
CTGAGGGAAA	TCGACAAAAT	TGTGGGGCAA	TTAATGGATG	1080
GACTGAAACA	ACTAAAACTG	CATCGGTGTG	TCAACGTCAT	1120
CTTTGTCTGA	GACCATGGAA	TGGAAGATGT	CACATGTGAT	1160
AGAACTGAGT	TCTTGAGTAA	TTACCTAACT	AATGTGGATG	1200
ATATTACTTT	AGTGCCTGGA	ACTCTAGGAA	TTCGATCCAA	1240
ATTTAGCAAC	AATGCTAAAT	ATGACCCCAA	AGCCATTATT	1280
GCCAATCTCA	CGTGTAACAAA	ACCAGATCAG	CACTTTAAGC	1320
CTTACTTGAA	ACAGCACCTT	CCCAAACGTT	TGCACTATGC	1360
CAACAACAGA	AGAATTGAGG	ATATCCATTT	ATTGGTGGAA	1400
CGCAGATGGC	ATGTTGCAAG	GAAACCTTTG	GATGTTTATA	1440
AGAAACCATC	AGGAAAATGC	TTTTTCCAGG	GAGACCACGG	1480
ATTTGATAAC	AAGGTCAACA	GCATGCAGAC	TGTTTTTGTA	1520
GGTTATGGCC	CAACATTTAA	GTACAAGACT	AAAGTGCCTC	1560
CATTTGAAAA	CATTGAACTT	TACAATGTTA	TGTGTGATCT	1600
CCTGGGATTG	AAGCCAGCTC	CTAATAATGG	GACCCATGGA	1640
AGTTTGAATC	ATCTCCTGCG	CACTAATACC	TTCAGGCCAA	1680
CCATGCCAGA	GGAAGTTACC	AGACCCAATT	ATCCAGGGAT	1720
TATGTACCTT	CAGTCTGATT	TTGACCTGGG	CTGCACTTGT	1760
GATGATAAGG	TAGAGCCAAA	GAACAAGTTG	GATGAACTCA	1800
ACAAACGGCT	TCATACAAAA	GGGTCTACAG	AAGAGAGACA	1840
CCTCCTCTAT	GGGCGACCTG	CAGTGCTTTA	TCGGACTAGA	1880
TATGATGTCT	TATATCACAC	TGACTTTGAA	AGTGGTTATA	1920
GTGAAATATT	CCTAATGCCA	CTCTGGACAT	CATATACTGT	1960
TTCCAAACAG	GCTGAGGTTT	CCAGCGTTCC	TGACCATCTG	2000
ACCAGTTGCG	TCCGGCCTGA	TGTCCGTGTT	TCTCCGAGTT	2040
TCAGTCAGAA	CTGTTTGGCC	TACAAAAATG	ATAAGCAGAT	2080
GTCCTACGGA	TTCTCTTTTC	CTCCTTATCT	GAGCTCTTCA	2120
CCAGAGGCTA	AATATGATGC	ATTCCTTGTA	ACCAATATGG	2160
TTCCAATGTA	TCCTGCTTTC	AAACGGGTCT	GGAATTATTT	2200
CCAAAGGGTA	TTGGTGAAGA	AATATGCTTC	GGAAAGAAAT	2240
GGAGTTAACG	TGATAAGTGG	ACCAATCTTC	GACTATGACT	2280
ATGATGGCTT	ACATGACACA	GAAGACAAAA	TAAAACAGTA	2320
CGTGGAAGGC	AGTTCCATTC	CTGTTCCAAC	TCACTACTAC	2360
AGCATCATCA	CCAGCTGTCT	GGATTTCACT	CAGCCTGCCG	2400
ACAAGTGTGA	CGGCCCTCTC	TCTGTGTCTT	CCTTCATCCT	2440
CCGTCAACGG	CCTGACAACG	AGGAGAGCTG	CAATAGCTCA	2480
GAGGACGAAT	CAAAATGGGT	AGAAGAACCT	ATGAAGATGC	2520
ACACGGCTAG	GGTGCGTGAC	ATTGAACATC	TCACCAGCCT	2560
GGACTTCTTC	CGAAAGACCA	GCCGCAGCTA	CCCAGAAATC	2600
CTGACACTCA	AGACATACCT	GCATACATAT	GAGAGCGAGA	2640
TTTAACTTTC	TGAGCATCTG	CAGTACAGTC	TTATCAACTG	2680
GTTGTATATT	TTTATATTGT	TTTTGTATTT	ATTAATTTGA	2720

AACCAGGACA	TTAAAAATGT	TAGTATTTTA	ATCCTGTACC	2760
AAATCTGACA	TATTATGCCT	GAATGACTCC	ACTGTTTTTC	2800
TCTAATGCTT	GATTTAGGTA	GCCTTGTGTT	CTGAGTAGAG	2840
CTTGTAATAA	ATACTGCAGC	TTGAGTTTTT	AGTGGAAGCT	2880
TCTAAATGGT	GCTGCAGATT	TGATATTTGC	ATTGAGGAAA	2920
TATTAATTTT	CCAATGCACA	GTTGCCACAT	TTAGTCCTGT	2960
ACTGTATGGA	AACACTGATT	TTGTAAAGTT	GCCTTTATTT	3000
GCTGTAACT	GTAACTATG	ACAGATATAT	TTAAGCCTTA	3040
TAAACCAATC	TTAAACATAA	TAAATCACAC	ATTCAGTTTT	3080
TTCTGGTAAA	AAAAAAAAAA	AAAA		3104

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: N-tera 2D1 ATX protein
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met	Ala	Arg	Arg	Ser	Ser	Phe	Gln	Ser	Cys	Gln	Ile	Ile	Ser	Leu	Phe
1				5					10					15	
Thr	Phe	Ala	Val	Gly	Val	Asn	Ile	Cys	Leu	Gly	Phe	Thr	Ala	His	Arg
			20					25					30		
Ile	Lys	Arg	Ala	Glu	Gly	Trp	Glu	Glu	Gly	Pro	Pro	Thr	Val	Leu	Ser
		35				40						45			
Asp	Ser	Pro	Trp	Thr	Asn	Ile	Ser	Gly	Ser	Cys	Lys	Gly	Arg	Cys	Phe
	50				55					60					
Glu	Leu	Gln	Glu	Ala	Gly	Pro	Pro	Asp	Cys	Arg	Cys	Asp	Asn	Leu	Cys
65				70					75					80	
Lys	Ser	Tyr	Thr	Ser	Cys	Cys	His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys
			85					90					95		
Thr	Ala	Arg	Ala	Trp	Glu	Cys	Thr	Lys	Asp	Arg	Cys	Gly	Glu	Val	Arg
			100					105					110		
Asn	Glu	Glu	Asn	Ala	Cys	His	Cys	Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly
		115				120						125			
Asp	Cys	Cys	Thr	Asn	Tyr	Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp
	130				135					140					
Val	Asp	Asp	Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala	Glu	Cys	Pro	Ala	Gly
145				150					155						160

Phe	Val	Arg	Pro	Pro	Leu	Ile	Ile	Phe	Ser	Val	Asp	Gly	Phe	Arg	Ala
				165					170					175	
Ser	Tyr	Met	Lys	Lys	Gly	Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu
			180					185					190		
Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	His	Met	Arg	Pro	Val	Tyr	Pro	Thr
		195					200					205			
Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr	Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu
	210					215					220				
Ser	His	Gly	Ile	Val	Gly	Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala
225					230					235					240
Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His	Arg	Trp	Trp	Gly
				245					250					255	
Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala	Thr	Lys	Gln	Arg	Gly	Glu	Ser	Trp
			260					265					270		
Asn	Ile	Leu	Leu	Val	Cys	Cys	His	Pro	Ser	Arg	Ala	Glu	Ile	Leu	Thr
		275					280					285			
Ile	Leu	Gln	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg	Leu	Arg	Ser	Met
	290					295					300				
Pro	Ser	Ile	Leu	Ser	Asn	Leu	Ile	Ser	Leu	Asp	Thr	Asn	Met	Pro	Phe
305					310					315					320
Gly	Pro	Glu	Met	Thr	Asn	Pro	Leu	Arg	Glu	Ile	Asp	Lys	Ile	Val	Gly
				325					330					335	
Gln	Leu	Met	Asp	Gly	Leu	Lys	Gln	Leu	Lys	Leu	His	Arg	Cys	Val	Asn
			340					345					350		
Val	Ile	Phe	Val	Gly	Asp	His	Gly	Met	Glu	Asp	Val	Thr	Cys	Asp	Arg
		355					360					365			
Thr	Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val	Asp	Asp	Ile	Thr	Leu
	370					375					380				
Val	Pro	Gly	Thr	Leu	Gly	Ile	Arg	Ser	Lys	Phe	Ser	Asn	Asn	Ala	Lys
385					390					395					400
Tyr	Asp	Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	Thr	Cys	Lys	Lys	Pro	Asp
				405					410					415	
Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His	Leu	Pro	Lys	Arg	Leu	His
			420					425					430		
Tyr	Ala	Asn	Asn	Arg	Arg	Ile	Glu	Asp	Ile	His	Leu	Leu	Val	Glu	Arg
		435					440					445			
Arg	Trp	His	Val	Ala	Arg	Lys	Pro	Leu	Asp	Val	Tyr	Lys	Lys	Pro	Ser
	450					455					460				
Gly	Lys	Cys	Phe	Phe	Gln	Gly	Asp	His	Gly	Phe	Asp	Asn	Lys	Val	Asn
465					470					475					480
Ser	Met	Gln	Thr	Val	Phe	Val	Gly	Tyr	Gly	Pro	Thr	Phe	Lys	Tyr	Lys
				485					490					495	
Thr	Lys	Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	Leu	Tyr	Asn	Val	Met	Cys
			500					505					510		
Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn	Asn	Gly	Thr	His	Gly	Ser
		515					520					525			
Leu	Asn	His	Leu	Leu	Arg	Thr	Asn	Thr	Phe	Arg	Pro	Thr	Met	Pro	Glu
	530					535					540				
Glu	Val	Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	Met	Tyr	Leu	Gln	Ser	Asp
445					450					555					560
Phe	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys	Val	Glu	Pro	Lys	Asn	Lys
				565					570					575	
Leu	Asp	Glu	Leu	Asn	Lys	Arg	Leu	His	Thr	Lys	Gly	Ser	Thr	Glu	Glu
			580					585						590	



Arg	His	Leu	Leu	Tyr	Gly	Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr	Arg	Tyr
		595					600					605			
Asp	Val	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser	Gly	Tyr	Ser	Glu	Ile	Phe
	610					615					620				
Leu	Met	Pro	Leu	Trp	Thr	Ser	Tyr	Thr	Val	Ser	Lys	Gln	Ala	Glu	Val
625					630					635					640
Ser	Ser	Val	Pro	Asp	His	Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp	Val	Arg
				645					650					655	
Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu	Ala	Tyr	Lys	Asn	Asp	Lys
			660					665					670		
Gln	Met	Ser	Tyr	Gly	Phe	Leu	Phe	Pro	Pro	Tyr	Leu	Ser	Ser	Ser	Pro
		675					680					685			
Glu	Ala	Lys	Tyr	Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro	Met	Tyr
	690					695					700				
Pro	Ala	Phe	Lys	Arg	Val	Trp	Asn	Tyr	Phe	Gln	Arg	Val	Leu	Val	Lys
705					710					715					720
Lys	Tyr	Ala	Ser	Glu	Arg	Asn	Gly	Val	Asn	Val	Ile	Ser	Gly	Pro	Ile
				725					730					735	
Phe	Asp	Tyr	Asp	Tyr	Asp	Gly	Leu	His	Asp	Thr	Glu	Asp	Lys	Ile	Lys
			740				745						750		
Gln	Tyr	Val	Glu	Gly	Ser	Ser	Ile	Pro	Val	Pro	Thr	His	Tyr	Tyr	Ser
		755					760					765			
Ile	Ile	Thr	Ser	Cys	Leu	Asp	Phe	Thr	Gln	Pro	Ala	Asp	Lys	Cys	Asp
	770					775					780				
Gly	Pro	Leu	Ser	Val	Ser	Ser	Phe	Ile	Leu	Arg	His	Arg	Pro	Asp	Asn
785					790					795					800
Glu	Glu	Ser	Cys	Asn	Ser	Ser	Glu	Asp	Glu	Ser	Lys	Trp	Val	Glu	Glu
				805					810					815	
Leu	Met	Lys	Met	His	Thr	Ala	Arg	Val	Arg	Asp	Ile	Glu	His	Leu	Thr
			820					825					830		
Ser	Leu	Asp	Phe	Phe	Arg	Lys	Thr	Ser	Arg	Ser	Tyr	Pro	Glu	Ile	Leu
		835					840					845			
Thr	Leu	Lys	Thr	Tyr	Leu	His	Thr	Tyr	Glu	Ser	Glu	Ile			
	850					855					860				

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3251
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (ix) FEATURE:
  - (A) NAME/KEY: A2058 ATX cDNA
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CGTGAAGGCA	AAGAGAACAC	GCTGCAAAAAG	GCTTCCAAGA	40
ATCCTCGACA	TGGCAAGGAG	GAGCTCGTTC	CAGTCGTGTC	80
AGATAATATC	CCTGTTCACT	TTTGCCGTTG	GAGTCAGTAT	120
CTGCTTAGGA	TTCAGTGCAC	ATCGAATTAA	GAGAGCAGAA	160
GGATGGGAGG	AAGGTCCCTC	TACAGTGCTA	TCAGACTCCC	200
CCTGGACCAA	CATCTCCGGA	TCTTGCAAGG	GCAGGTGCTT	240
TGAACTTCAA	GAGGCTGGAC	CTCCTGATTG	TCGCTGTGAC	280
AACTTGTGTA	AGAGCTATAC	CAGTTGCTGC	CATGACTTTG	320
ATGAGCTGTG	TTTGAAGACA	GCCCGTGGCT	GGGAGTGTAC	360
TAAGGACAGA	TGTGGAGAAG	TCAGAAATGA	AGAAAATGCC	400
TGTCAGTGCT	CAGAGGACTG	CTTGCCAGG	GGAGACTGCT	440
GTACCAATTA	CCAAGTGGTT	TGCAAAGGAG	AGTCGCATTG	480
GGTTGATGAT	GACTGTGAGG	AAATAAAGGC	CGCAGAATGC	520
CCTGCAGGGT	TTGTTCGCCC	TCCATTAATC	ATCTTCTCCG	560
TGGATGGCTT	CCGTGCATCA	TACATGAAGA	AAGGCAGCAA	600
AGTCATGCCT	AATATTGAAA	AACTAAGGTC	TTGTGGCACA	640
CACTCTCCCT	ACATGAGGCC	GGTGTACCCA	ACTAAAACCT	680
TTCTTAACCT	ATACACTTTG	GCCACTGGGC	TATATCCAGA	720
ATCACATGGA	ATTGTTGGCA	ATTCAATGTA	TGATCCTGTA	760
TTTGATGCCA	CTTTTCATCT	GCGAGGGCGA	GAGAAATTTA	800
ATCATAGATG	GTGGGGAGGT	CAACCGCTAT	GGATTACAGC	840
CACCAAGCAA	GGGGTGAAAG	CTGGAACATT	CTTTTGCTCT	880
GTTGTCATCC	CTCACGAGCG	GAGAATATTA	ACCATATTGC	920
GGTGGCTCAC	CCTGCCAGAT	CATGAGAGGC	CTTCGGTCTA	960
TGCCTTCTAT	TCTGAGCAAC	CTGATTTCTC	TGGACACAAA	1000
TATGGCCCTT	TCGGCCCTGA	GGAGAGTAGT	TATGGCTCAC	1040
CTTTTACTCC	GGCTAAGAGA	CCTAAGAGGA	AAGTTGCCCC	1080
TAAGAGGAGA	CAGGAAAGAC	CAGTTGCTCC	TCCAAAGAAA	1120
AGAAGAAGAA	AAATACATAG	GATGGATCAT	TATGCTGCGG	1160
AAACTCGTCA	GGACAAAATG	ACAAATCCTC	TGAGGGAAAT	1200
CGACAAAATT	GTGGGGCAAT	TAATGGATGG	ACTGAAACAA	1240
CTAAAACTGC	GTCGGTGTGT	CAACGTCATC	TTTGTGCGAG	1280
ACCATGGAAT	GGAAGATGTC	ACATGTGATA	GAAGTGTGTT	1320
CTTGAGTAAT	TACCTAACTA	ATGTGGATGA	TATTACTTTA	1360
GTGCCTGGAA	CTCTAGGAAG	AATTCGATCC	AAATTTAGCA	1400
ACAATGCTAA	ATATGACCCC	AAAGCCATTA	TTGCCAATCT	1440
CACGTGTAAA	AAACCAGATC	AGCACTTTAA	GCCTTACTTG	1480
AAACAGCACC	TTCCCAAACG	TTTGCACTAT	GCCAACAACA	1520
GAAGAATTGA	GGATATCCAT	TTATTGGTGG	AACGCAGATG	1560
GCATGTTGCA	AGGAAACCTT	TGGATGTTTA	TAAGAAACCA	1600
TCAGGAAAAT	GCTTTTTTCCA	GGGAGACCAC	GGATTTGATA	1640
ACAAGGTCAA	CAGCATGCAG	ACTGTTTTTG	TAGGTTATGG	1680
CCCAACATTT	AAGTACAAGA	CTAAAGTGCC	TCCATTTGAA	1720
AACATTGAAC	TTTACAATGT	TATGTGTGAT	CTCCTGGGAT	1760
TGAAGCCAGC	TCCTAATAAT	GGGACCCATG	GAAGTTTGAA	1800
TCATCTCCTG	CGCACTAATA	CCTTCAGGCC	AACCATGCCA	1840
GAGGAAGTTA	CCAGACCCAA	TTATCCAGGG	ATTATGTACC	1880
TTCAGTCTGA	TTTTGACCTG	GGCTGCACTT	GTGATGATAA	1920
GGTAGAGCCA	AAGAACAAGT	TGGATGAACT	CAACAAACGG	1960
CTTCATACAA	AAGGGTCTAC	AGAAGAGAGA	CACCTCCTCT	2000

ATGGGCGACC	TGCAGTGCTT	TATCGGACTA	GATATGATAT	2040
CTTATATCAC	ACTGACTTTG	AAAGTGGTTA	TAGTGAAATA	2080
TTCCTAATGC	TACTCTGGAC	ATCATATACT	GTTTCCAAAC	2120
AGGCTGAGGT	TTCCAGCGTT	CCTGACCATC	TGACCAGTTG	2160
CGTCCGGCCT	GATGTCCGTG	TTTCTCCGAG	TTTCAGTCAG	2200
AACTGTTTGG	CCTACAAAAA	TGATAAGCAG	ATGTCCTACG	2240
GATTCCCTCTT	TCCTCCTTAT	CTGAGCTCTT	CACCAGAGGC	2280
TAAATATGAT	GCATTCCCTG	TAACCAATAT	GGTTCCAATG	2320
TATCCTGCTT	TCAAACGGGT	CTGGAATTAT	TTCCAAAGGG	2360
TATTGGTGAA	GAAATATGCT	TCGGAAAGAA	ATGGAGTTAA	2400
CGTGATAAGT	GGACCAATCT	TCGACTATGA	CTATGATGGC	2440
TTACATGACA	CAGAAGACAA	AATAAAACAG	TACGTGGAAG	2480
GCAGTTCCAT	TCCTGTTCCA	ACTCACTACT	ACAGCATCAT	2520
CACCAGCTGT	CTGGATTTC	CTCAGCCTGC	CGACAAGTGT	2560
GACGGCCCTC	TCTCTGTGTC	CTCCTTTCATC	CTGCCTCACC	2600
GGCCTGACAA	CGAGGAGAGC	TGCAATAGCT	CAGAGGACGA	2640
ATCAAAATGG	GTAGAAGAAC	TCATGAAGAT	GCACACAGCT	2680
AGGGTGCGTG	ACATTGAACA	TCTCACCAGC	CTGGACTTCT	2720
TCCGAAAGAC	CAGCCGCAGC	TACCCAGAAA	TCCTGACACT	2760
CAAGACATAC	CTGCATACAT	ATGAGAGCGA	GATTTAACTT	2800
TCTGAGCATC	TGCAGTACAG	TCTTATCAAC	TGGTTGTATA	2840
TTTTTATATT	GTTTTTGTAT	TTATTAATTT	GAAACCAGGA	2880
CATTAAAAAT	GTTAGTATTT	TAATCCTGTA	CCAAATCTGA	2920
CATATTATGC	CTGAATGACT	CCACTGTTTT	TCTCTAATGC	2960
TTGATTTAGG	TAGCCTTGTG	TTCTGAGTAG	AGCTTGTAAT	3000
AAATACTGCA	GCTTGAGAAA	AAGTGGAAGC	TTCTAAATGG	3040
TGCTGCAGAT	TTGATATTTG	CATTGAGGAA	ATATTAATTT	3080
TCCAATGCAC	AGTTGCCACA	TTTAGTCCTG	TACTGTATGG	3120
AAACACTGAT	TTTGTAAGT	TGCCTTTATT	TGCTGTTAAC	3160
TGTTAACTAT	GACAGATATA	TTTAAGCCTT	ATAAACCAAT	3200
CTTAAACATA	ATAAATCACA	CATTCAGTTT	TAAAAAATAA	3240
AAAAAAAAAA	A			3251

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(ix) FEATURE:

- (A) NAME/KEY: A2058 ATX protein
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Ala	Arg	Arg	Ser	Ser	Phe	Gln	Ser	Cys	Gln	Ile
1				5					10		
Ile	Ser	Leu	Phe	Thr	Phe	Ala	Val	Gly	Val	Ser	Ile
		15					20				
Cys	Leu	Gly	Phe	Thr	Ala	His	Arg	Ile	Lys	Arg	Ala
25					30					35	
Glu	Gly	Trp	Glu	Glu	Gly	Pro	Pro	Thr	Val	Leu	Ser
			40					45			
Asp	Ser	Pro	Trp	Thr	Asn	Ile	Ser	Gly	Ser	Cys	Lys
	50				55					60	
Gly	Arg	Cys	Phe	Glu	Leu	Gln	Glu	Ala	Gly	Pro	Pro
			65						70		
Asp	Cys	Arg	Cys	Asp	Asn	Leu	Cys	Lys	Ser	Tyr	Thr
		75					80				
Ser	Cys	Cys	His	Asp	Phe	Asp	Glu	Leu	Cys	Leu	Lys
85					90					95	
Thr	Ala	Arg	Gly	Trp	Glu	Cys	Thr	Lys	Asp	Arg	Cys
			100					105			
Gly	Glu	Val	Arg	Asn	Glu	Glu	Asn	Ala	Cys	His	Cys
	110				115					120	
Ser	Glu	Asp	Cys	Leu	Ala	Arg	Gly	Asp	Cys	Cys	Thr
			125						130		
Asn	Tyr	Gln	Val	Val	Cys	Lys	Gly	Glu	Ser	His	Trp
	135						140				
Val	Asp	Asp	Asp	Cys	Glu	Glu	Ile	Lys	Ala	Ala	Glu
145					150					155	
Cys	Pro	Ala	Gly	Phe	Val	Arg	Pro	Pro	Leu	Ile	Ile
			160					165			
Phe	Ser	Val	Asp	Gly	Phe	Arg	Ala	Ser	Tyr	Met	Lys
	170				175					180	
Lys	Gly	Ser	Lys	Val	Met	Pro	Asn	Ile	Glu	Lys	Leu
			185						190		
Arg	Ser	Cys	Gly	Thr	His	Ser	Pro	Tyr	Met	Arg	Pro
		195					200				
Val	Tyr	Pro	Thr	Lys	Thr	Phe	Pro	Asn	Leu	Tyr	Thr
205					210					215	
Leu	Ala	Thr	Gly	Leu	Tyr	Pro	Glu	Ser	His	Gly	Ile
			220					225			
Val	Gly	Asn	Ser	Met	Tyr	Asp	Pro	Val	Phe	Asp	Ala
	230					235				240	
Thr	Phe	His	Leu	Arg	Gly	Arg	Glu	Lys	Phe	Asn	His
			245						250		
Arg	Trp	Trp	Gly	Gly	Gln	Pro	Leu	Trp	Ile	Thr	Ala
		255					260				
Thr	Lys	Gln	Gly	Val	Lys	Ala	Gly	Thr	Phe	Phe	Trp
265					270					275	
Ser	Val	Val	Ile	Pro	His	Glu	Arg	Arg	Ile	Leu	Thr
			280					285			
Ile	Leu	Arg	Trp	Leu	Thr	Leu	Pro	Asp	His	Glu	Arg
	290					295				300	
Pro	Ser	Val	Tyr	Ala	Phe	Tyr	Ser	Glu	Gln	Pro	Asp
				305					310		

Phe	Ser	Gly	His	Lys	Tyr	Gly	Pro	Phe	Gly	Pro	Glu
		315					320				
Glu	Ser	Ser	Tyr	Gly	Ser	Pro	Phe	Thr	Pro	Ala	Lys
325					330					335	
Arg	Pro	Lys	Arg	Lys	Val	Ala	Pro	Lys	Arg	Arg	Gln
			340					345			
Glu	Arg	Pro	Val	Ala	Pro	Pro	Lys	Lys	Arg	Arg	Arg
	350					355					360
Lys	Ile	His	Arg	Met	Asp	His	Tyr	Ala	Ala	Glu	Thr
				365					370		
Arg	Gln	Asp	Lys	Met	Thr	Asn	Pro	Leu	Arg	Glu	Ile
		375					380				
Asp	Lys	Ile	Val	Gly	Gln	Leu	Met	Asp	Gly	Leu	Lys
385					390					395	
Gln	Leu	Lys	Leu	Arg	Arg	Cys	Val	Asn	Val	Ile	Phe
			400					405			
Val	Gly	Asp	His	Gly	Met	Glu	Asp	Val	Thr	Cys	Asp
	410					415					420
Arg	Thr	Glu	Phe	Leu	Ser	Asn	Tyr	Leu	Thr	Asn	Val
				425					430		
Asp	Asp	Ile	Thr	Leu	Val	Pro	Gly	Thr	Leu	Gly	Arg
		435					440				
Ile	Arg	Ser	Lys	Phe	Ser	Asn	Asn	Ala	Lys	Tyr	Asp
445					450					455	
Pro	Lys	Ala	Ile	Ile	Ala	Asn	Leu	Thr	Cys	Lys	Lys
			460					465			
Pro	Asp	Gln	His	Phe	Lys	Pro	Tyr	Leu	Lys	Gln	His
	470					475					480
Leu	Pro	Lys	Arg	Leu	His	Tyr	Ala	Asn	Asn	Arg	Arg
				485					490		
Ile	Glu	Asp	Ile	His	Leu	Leu	Val	Glu	Arg	Arg	Trp
		495					500				
His	Val	Ala	Arg	Lys	Pro	Leu	Asp	Val	Tyr	Lys	Lys
505					510					515	
Pro	Ser	Gly	Lys	Cys	Phe	Phe	Gln	Gly	Asp	His	Gly
			520					525			
Phe	Asp	Asn	Lys	Val	Asn	Ser	Met	Gln	Thr	Val	Phe
	530					535					540
Val	Gly	Tyr	Gly	Pro	Thr	Phe	Lys	Tyr	Lys	Thr	Lys
				545					550		
Val	Pro	Pro	Phe	Glu	Asn	Ile	Glu	Leu	Tyr	Asn	Val
		555					560				
Met	Cys	Asp	Leu	Leu	Gly	Leu	Lys	Pro	Ala	Pro	Asn
565					570					575	
Asn	Gly	Thr	His	Gly	Ser	Leu	Asn	His	Leu	Leu	Arg
			580					585			
Thr	Asn	Thr	Phe	Arg	Pro	Thr	Met	Pro	Glu	Glu	Val
	590					595					600
Thr	Arg	Pro	Asn	Tyr	Pro	Gly	Ile	Met	Tyr	Leu	Gln
			605						610		
Ser	Asp	Phe	Asp	Leu	Gly	Cys	Thr	Cys	Asp	Asp	Lys
		615					620				
Val	Glu	Pro	Lys	Asn	Lys	Leu	Asp	Glu	Leu	Asn	Lys
625					630					635	

Arg	Leu	His	Thr	Lys	Gly	Ser	Thr	Glu	Glu	Arg	His
			640					645			
Leu	Leu	Tyr	Gly	Arg	Pro	Ala	Val	Leu	Tyr	Arg	Thr
	650					655					660
Arg	Tyr	Asp	Ile	Leu	Tyr	His	Thr	Asp	Phe	Glu	Ser
			665						670		
Gly	Tyr	Ser	Glu	Ile	Phe	Leu	Met	Leu	Leu	Trp	Thr
		675					680				
Ser	Tyr	Thr	Val	Ser	Lys	Gln	Ala	Glu	Val	Ser	Ser
685					690					695	
Val	Pro	Asp	His	Leu	Thr	Ser	Cys	Val	Arg	Pro	Asp
			700					705			
Val	Arg	Val	Ser	Pro	Ser	Phe	Ser	Gln	Asn	Cys	Leu
	710					715					720
Ala	Tyr	Lys	Asn	Asp	Lys	Gln	Met	Ser	Tyr	Gly	Phe
			725						730		
Leu	Phe	Pro	Pro	Tyr	Leu	Ser	Ser	Ser	Pro	Glu	Ala
		735					740				
Lys	Tyr	Asp	Ala	Phe	Leu	Val	Thr	Asn	Met	Val	Pro
745					750					755	
Met	Tyr	Pro	Ala	Phe	Lys	Arg	Val	Trp	Asn	Tyr	Phe
			760					765			
Gln	Arg	Val	Leu	Val	Lys	Lys	Tyr	Ala	Ser	Glu	Arg
	770				775						780
Asn	Gly	Val	Asn	Val	Ile	Ser	Gly	Pro	Ile	Phe	Asp
			785						790		
Tyr	Asp	Tyr	Asp	Gly	Leu	His	Asp	Thr	Glu	Asp	Lys
		795					800				
Ile	Lys	Gln	Tyr	Val	Glu	Gly	Ser	Ser	Ile	Pro	Val
805					810					815	
Pro	Thr	His	Tyr	Tyr	Ser	Ile	Ile	Thr	Ser	Cys	Leu
			820					825			
Asp	Phe	Thr	Gln	Pro	Ala	Asp	Lys	Cys	Asp	Gly	Pro
	830					835					840
Leu	Ser	Val	Ser	Ser	Phe	Ile	Leu	Pro	His	Arg	Pro
			845						850		
Asp	Asn	Glu	Glu	Ser	Cys	Asn	Ser	Ser	Glu	Asp	Glu
		855					860				
Ser	Lys	Trp	Val	Glu	Glu	Leu	Met	Lys	Met	His	Thr
865					870					875	
Ala	Arg	Val	Arg	Asp	Ile	Glu	His	Leu	Thr	Ser	Leu
			880					885			
Asp	Phe	Phe	Arg	Lys	Thr	Ser	Arg	Ser	Tyr	Pro	Glu
	890					895					900
Ile	Leu	Thr	Leu	Lys	Thr	Tyr	Leu	His	Thr	Tyr	
				905					910		
Glu	Ser	Glu	Ile								
		916									